

Involvement of FGFR4 Gene Variants on the Clinicopathological Severity in Urothelial Cell Carcinoma

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Table 1. Genotype distributions of Fibroblast growth factor receptor 4 (FGFR4) gene polymorphisms in 856 Controls and 272 patients had primary bladder UCC.

| Variable | Controls (N = 856) n (%) | Patients (N = 272) n (%) | OR (95% CIs) | AOR (95% CIs) |
|------------------|-----------------------------|-----------------------------|----------------------|---------------------|
| rs2011077 | | | | |
| TT | 221 (25.8%) | 71 (26.1%) | 1.000 (reference) | 1.000 (reference) |
| TC | 418 (48.8%) | 139 (51.1%) | 1.035 (0.745–1.438) | 0.973 (0.621–1.525) |
| CC | 217 (25.4%) | 62 (22.8%) | 0.889 (0.603–1.312) | 0.815 (0.478–1.391) |
| TC+CC | 635 (74.2%) | 201 (73.9%) | 0.985 (0.722–1.345) | 0.919 (0.602–1.403) |
| rs351855 | | | | |
| GG | 242 (28.3%) | 74 (27.2%) | 1.000 (reference) | 1.000 (reference) |
| GA | 426 (49.7%) | 139 (51.1%) | 1.067 (0.772–1.474) | 1.167 (0.751–1.815) |
| AA | 188 (22.0%) | 59 (21.7%) | 1.026 (0.694–1.518) | 0.983 (0.569–1.697) |
| GA+AA | 614 (71.7%) | 198 (72.8%) | 1.055 (0.777–1.432) | 1.111 (0.730–1.691) |
| rs7708357 | | | | |
| GG | 838 (97.9%) | 266 (97.8%) | 1.000 (reference) | 1.000 (reference) |
| GA | 17 (2.0%) | 5 (1.8%) | 0.927 (0.339–2.535) | 1.518 (0.463–4.975) |
| AA | 1 (0.1%) | 1 (0.4%) | 3.150 (0.196–50.540) | --- |
| AG+AA | 18 (2.1%) | 6 (2.2%) | 1.050 (0.413–2.673) | 2.013 (0.672–6.029) |
| rs1966265 | | | | |
| AA | 221 (25.8%) | 68 (25.0%) | 1.000 (reference) | 1.000 (reference) |
| AG | 420 (49.1%) | 142 (52.2%) | 0.937 (0.633–1.387) | 0.861 (0.498–1.489) |
| GG | 215 (25.1%) | 62 (22.8%) | 1.099 (0.789–1.531) | 1.124 (0.713–1.772) |
| AG+GG | 635 (74.2%) | 204 (75.0%) | 1.044 (0.763–1.430) | 1.034 (0.671–1.594) |

CIs: confidence intervals; OR: odds ratio with their 95% confidence intervals were estimated by logistic regression models. AOR: adjusted odds ratio with their 95% confidence intervals were estimated by multiple logistic regression models after controlling for age, gender, and tobacco consumption.

Table S2. Genotype distributions of Fibroblast growth factor receptor 4 (FGFR4) gene polymorphisms in 856 Controls and 156 primary upper tract UC.

| Variable | Controls (N = 856) n (%) | Patients (N = 156) n (%) | OR (95% CIs) | AOR (95% CIs) |
|------------------|-----------------------------|-----------------------------|---------------------|---------------------|
| rs2011077 | | | | |
| TT | 221 (25.8%) | 39 (25.0%) | 1.000 (reference) | 1.000 (reference) |
| TC | 418 (48.8%) | 85 (54.5%) | 1.152 (0.763–1.741) | 1.113 (0.734–1.689) |
| CC | 217 (25.4%) | 32 (20.5%) | 0.836 (0.505–1.383) | 0.821 (0.494–1.365) |
| TC+CC | 635 (74.2%) | 117 (75.0%) | 1.044 (0.705–1.547) | 1.728 (0.901–3.314) |
| rs351855 | | | | |
| GG | 242 (28.3%) | 40 (25.6%) | 1.000 (reference) | 1.000 (reference) |
| GA | 426 (49.7%) | 83 (53.2%) | 1.179 (0.783–1.774) | 1.259 (0.832–1.906) |
| AA | 188 (22.0%) | 33 (21.2%) | 1.062 (0.645–1.749) | 1.096 (0.662–1.813) |
| GA+AA | 614 (71.7%) | 116 (74.4%) | 1.143 (0.775–1.686) | 1.660 (0.888–3.106) |
| rs7708357 | | | | |
| GG | 838 (97.9%) | 150 (96.2%) | 1.000 (reference) | 1.000 (reference) |

| | | | | |
|------------------|-------------|-------------|----------------------|---------------------|
| GA | 17 (2.0%) | 5 (3.2%) | 1.643 (0.597–4.521) | 1.678 (0.602–4.678) |
| AA | 1 (0.1%) | 1 (0.6%) | 5.587 (0.348–89.804) | |
| AG+AA | 18 (2.1%) | 6 (3.8%) | 1.862 (0.727–4.768) | 2.055 (0.514–8.226) |
| rs1966265 | | | | |
| AA | 221 (25.8%) | 39 (25.0%) | 1.000 (reference) | 1.000 (reference) |
| AG | 420 (49.1%) | 84 (53.8%) | 0.870 (0.527–1.434) | 0.851 (0.513–1.409) |
| GG | 215 (25.1%) | 33 (21.2%) | 1.133 (0.750–1.713) | 1.098 (0.723–1.666) |
| AG+GG | 635 (74.2%) | 117 (75.0%) | 1.044 (0.705–1.547) | 1.728 (0.901–3.314) |

CIs: confidence intervals; OR: odds ratio with their 95% confidence intervals were estimated by logistic regression models. AOR: adjusted odds ratio with their 95% confidence intervals were estimated by multiple logistic regression models after controlling for age, gender, and tobacco consumption.